We Claim:

1. A method for inferring a gene network, comprising

(a) providing an inferential model of possible gene networks of an organism including defining a search space;

(b) selecting a biologically relevant subspace of said search space; and

(c) calculating an optimal solution in said selected subspace by repeatedly applying an algorithm that computes small gene networks optimally.

2. The method of claim 1, wherein said inferential model is a Bayesian network estimation model.

3. The method of claim 1, wherein said biologically relevant subspace includes genes relating to a metabolic pathway of said organism.

4. The method of claim 1, wherein said algorithm comprises the steps:

(a) compute $F(g,\phi) = s(g,\phi)$ for all $g \in G$;

(b) for all $A \subseteq G$, $A \neq \phi$ and all $g \in G$ compute $F(g, A)$ as $\min\{s(g,A), \min_{a \in A} F(g, A-\{a\})\}$;

(c) set $M(\phi)=\phi$;

(d) for all $A \subseteq G$, $A \neq \phi$, do the following steps:

(i) compute $g^* = \arg\min_{g \subset A} (F(g,A-\{g\})+Q^{A-\{g\}}(M(A-\{g\})))$; and

(ii) for all $1 \leq i < |A|$, set $M(A)(i)=M(A-\{g^*\})(i)$, and $M(A)(|A|) = g^*$; and

(e) return $Q^G(M(G))$.

5. The method of claim 4, wherein said algorithm is modified according to the steps of:

(a) in the computation of F in Step 1 and Step 2, compute only $F(g,A)$ for all $g \in S_i$ and all $A \subseteq C_g$; and

(b). replace the term $F(g, A - \{g\})$ in Step 4a by $F(g, (C_g = S_i) \bigcup (C_g \bigcap A))$.

6. The method of claim 1, wherein an optimal network N has a definition: $score(N) = \sum_{g \in G} s(g, P^N(g))$.

7. The method of claim 1, wherein said algorithm comprises the steps:

(a) cluster genes in G such that no cluster is larger than c genes;

(b) sort the clusters by decreasing size: $C_1, \ldots, C_n$;

(c) for each $i \in \{1, \ldots, n\}$ and for each $g \in C_i$, select up to m candidate parents from $C_1 \bigcup \ldots \bigcup C_n$; and

(d) compute an optimal gene network model using Theorem 1.2.

8. The method of claim 1, wherein said algorithm comprises the steps:

(a) group genes in G in groups C_i with $|C_i| \leq c$ and sort them according to biological knowledge: $C_{1, \ldots,} C_n$;

(b) for each $i \in \{1, \ldots, n\}$ and for each gene $g \in C_i$, select up to m candidate parents from $C_1 \bigcup \ldots \bigcup C_i$; and

(c) compute an optimal gene network model using Theorem 2.

9. The method of claim 1, wherein said algorithm comprises the steps:

(a) compute $F(g,\phi) = s(g,\phi)$ for all $g \in G$;

(b) for all $A \subseteq G$, $A \neq \phi$ and all $g \in G$ compute $F(g, A)$ as $\min\{s(g,A), \min_{\bar{a} \in A} F(g, A-\{a\})\}$;

(cc) set $M(\phi)=\phi$;

(d) for all $A \subseteq G$, $A \neq \phi$, do the following two steps:

(i) compute $g^* = \arg\min_{g \subset A} (F(g, A-\{g\}) + Q^{A-\{g\}}(M(A-\{g\})))$; and

(ii) For all $1 \leq i < |A|$, set $M(A)(i) = M(A-\{g^*\})(i)$, and $M(A)(|A|) = g^*$; and

(e) return $Q^G(M(G))$.

10. The method of claim 1, wherein said algorithm comprises the steps:

(a) set $F^m(g,\phi,1) = \phi$, $S^m(g,\phi,1) = s(g,\phi)$ for all $g \in G$;

(b) for all $g \in G$, all $A \subseteq G$, $A \neq N$ and all $n \leq m$ do the following two steps:

(i) select $B^* \subseteq A$ from $\{B \subseteq A \mid B = A \vee B = F^m(g,A-\{h\},p), h \in A, p \leq m\}$ - $\{F^m(g,A,p) \mid p<n\}$ such that $s(g,B^*)$ is minimized; and

(ii) set $F^m(g,A,n)=B^*$, $S^m(g,A,n)=s(g,B^*)$;

(c) set $M^m(\phi,1)=\phi$ and $D^m(\phi,1)=\phi$;

(d) for all $A \subseteq G$, ϕ, and all $n \leq m$ do the following three steps:

(i) choose a triple $(g,p,q) \in A \times IN_{\leq m} \times IN_{\leq m}$ such that $score(Q^{A-\{g\}}(M^m(A-\{g\},p),D^m(A-\{g\},p)))+S^m(g,A-\{g\},q)$ is minimized and (g,p,q) induces a network different from $Q^A(M^m(A,r),D^m(A,r))$ for $r<n$;

(ii) set $M^m(A,n)(i)=M^m(A-\{g\},p)(i)$ for $i< |A|$, and $M^m(A,n)(|A|)=g$; and

(iii) let v denote $D^m(A-\{g\},p)$. Set $w \in IN^{|A|}$ as $w_i=v_i$ for all $I <|A|$ and $^w|A|=q$ and set $D^m(A,n) = w$; and

(e) return $Q^G(M^m(G,i),D^m(G,i))$ for all $i \leq m$.

11. The method of any of claims 1-10, wherein reliability of an enumerated gene network, comprising the steps:

(a) enumerate the most likely gene network models N_i, $1 \leq i \leq n$;

(b) for every g, $h \in 0G$, count the occurences of the edge (g,h) in the networks N_i;

(c) select all edges (g,h) with at least c occurrences;

(d) for all subsets M of the set of selected edges with $|M| = k$, count the networks including all edges in MI; and

(e) return all motives M with at least c occurences.

12. The method of any of claims 1-11, further comprising calculating a scoring function selected from the group consisting of BRNC score, BDe score and MDL score.

13. A method for determining a gene network as substantially described herein.

14. A storage medium containing results obtained using the method of any of claims 1-11.

15. A storage medium containing results obtained using a method as substantially described herein.

16. A system for determining gene network relationships, comprising:

an input device for providing quantitative expression data for genes of an organism;

a storage device adapted to receive quantitative expression data for genes of said organism;

a processor adapted to carryout a Bayesian network analysis of network relationships between said genes, thereby producing a data set reflecting said network relationships; and

an output device for displaying said data set of said network relationships.

17. A system for determining gene network relationships as substantially described herein.